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SCA2CAG

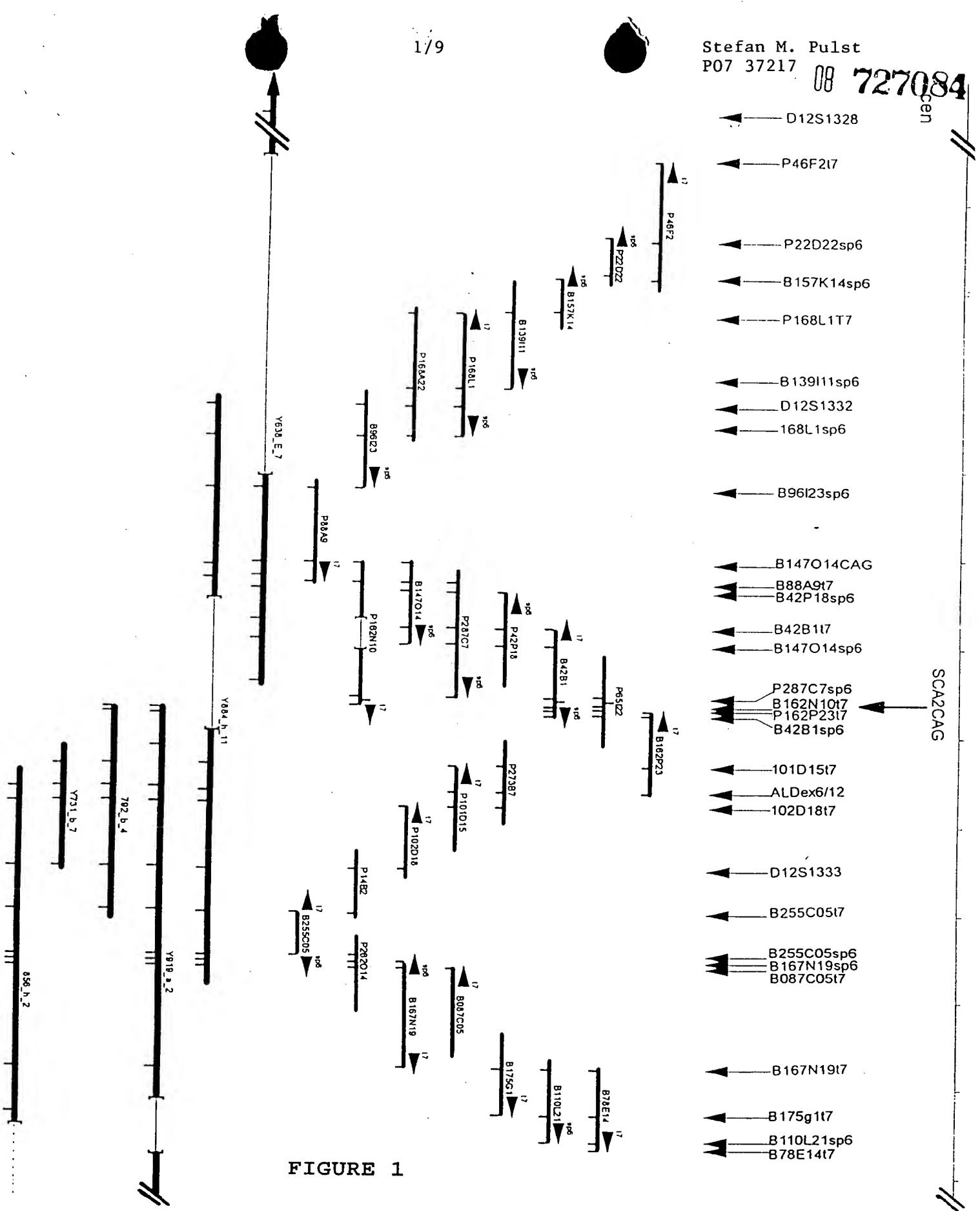


FIGURE 1

1 TTGGTAGCAACGGAAACAGCGGGCGGCGTTCGGCCGACTCCGGCGGCTCCGGTGT
61 TCGGCAGGGCTCCCCGCCCCCTCTGTCGTCTCTCCCCCTCAGCCAGGGCGGGCGCC
121 CTCCGGCCGGCCAAACCCAGGCTCCCCGCTCAGCAGCCGTGCGTCCCCAGGGCGTCCG
181 GCGTCTCTTGGCGCGCCCGGCTCCCGGCCTCTCCCCGCCCGGTGCGAACCCGGTGTATG
241 SCA2-A → AGCCCCCTCACCATGTCGCTGAAGCCCCAGCAGCAGCAGCAGCAGCAACAGCAGC
301 ← SCA2-B ← AGCAAGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGC
361 AGCCCCGGCGGGAAAGGGCTTCTAGCGTCGCCGCCAGCGCCCTCGCCGTCTCGCT
421 CAATCTCCTCGTCCTCAAGGACGGCTCCCTCTCGGTGAGCGCCGAAACCTCCGGCAAGC
481 GGAGGCCCCGGCCTGGGCAG GTGGGTGTGGCACCCCC

FIGURE 2

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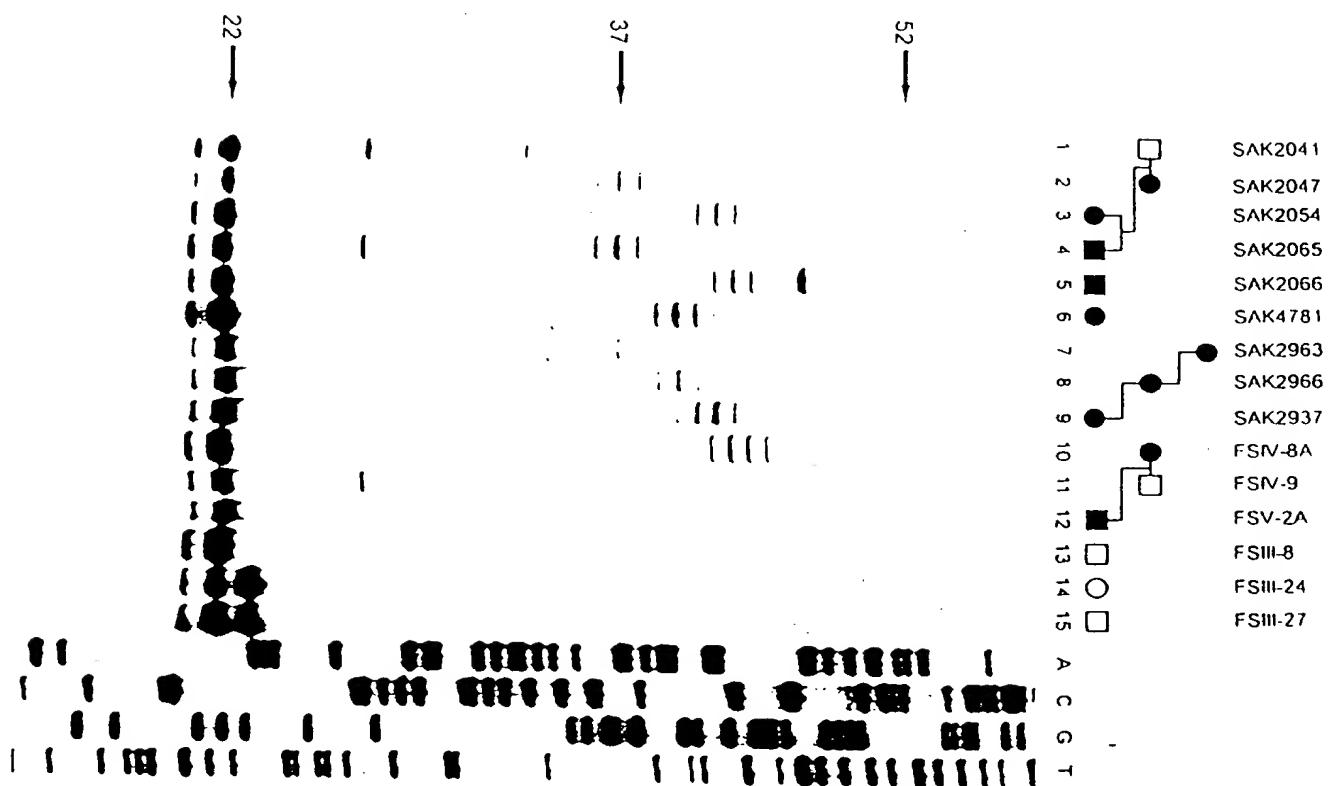


FIGURE 3

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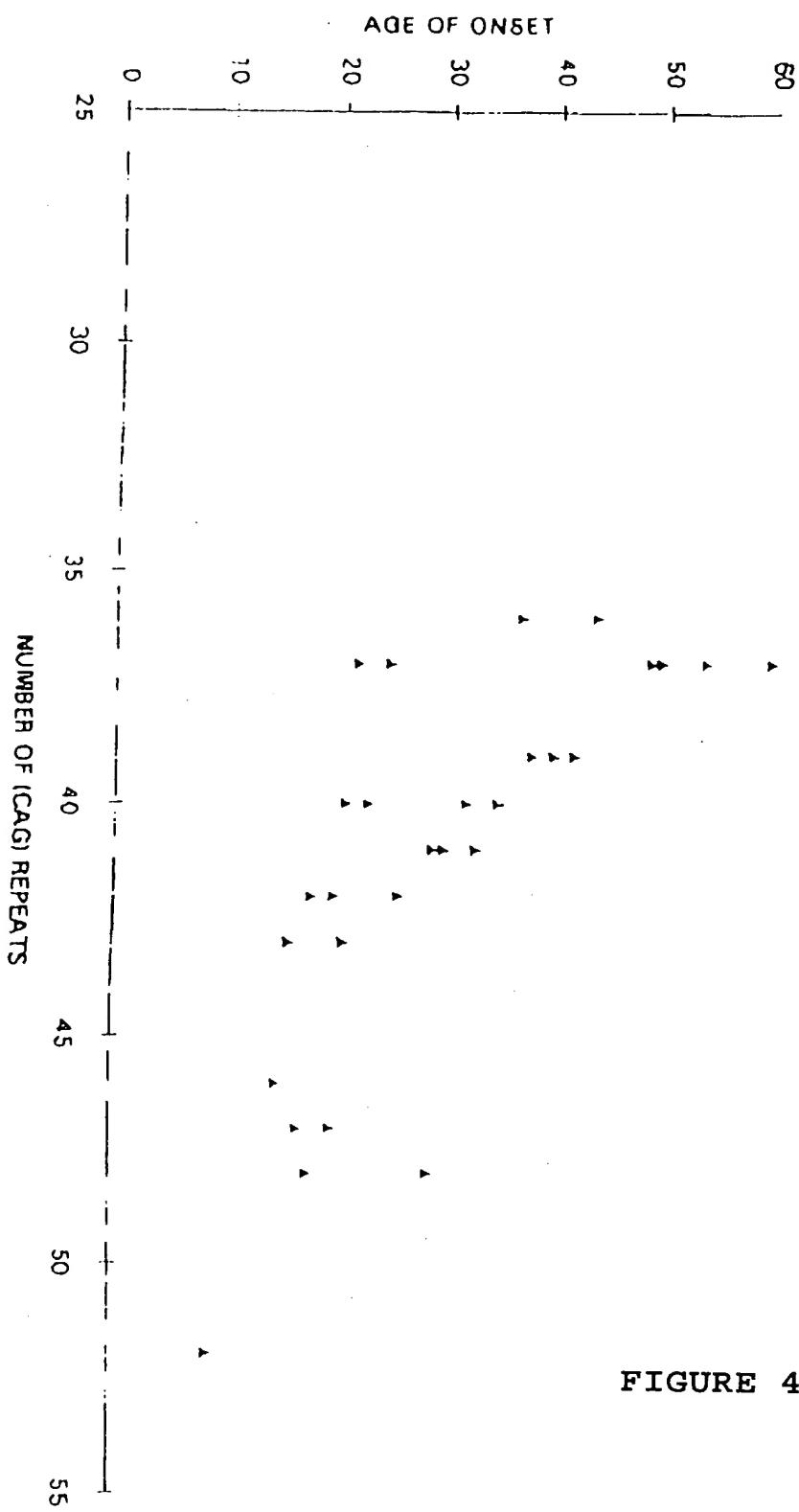


FIGURE 4

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F1.1-F1.7 5' AAA 3'

F2.1-F2.8 5' AAA 3'

S1 5' 3'

S2 5' 3'

300 bp

FIGURE 5

1	ACCCCCGAGAAAGCAACCCAGCGCGCCGCCGCTCCTCACGTGTCCCTCCCGCCCCGGG	60
61	GCCACCTCACGTTCTGCTTCCGTCTGACCCCTCCGACTTCGGTAAAGAGTCCTATCCG	120
121	CACCTCCGCTCCCACCCGGCGCTCGCGCGCCCGCCCTCCGATGCGCTCAGCGGCCGCA	180
1	M R S A A A	6
181	GCTCCTCGGAGTCCC GGCGTGGCCACCGAGTCTCGCCGCTTCGCCAGCCAGGTGGCCC	240
7	A P R S P A V A T E S R R F A A A R W P	26
241	GGGTGGCGCTCGCTCCAGCGGCCGGCGCGAGCGGGCGGGGGCGGCGGTGGCGCGGCC	300
27	G W R S L Q R P A R R S G R G G G G A A	46
301	CCGGGACCGTATCCCTCCGCCGCCCTCCCCGCCGGCCCCCTCCCTCCCG	360
47	P G P Y P S A A P P P P G P G P P P S R	66
361	CAGAGCTCGCCTCCCTCCGCCCTCAGACTGTTTGGTAGCAACGGCAACGGCGGCCGCG	420
67	Q S S P P S A S D C F G S N G N G G G A	86
421	TTTCGGCCCGGCTCCGGCGCTCCTTGGTCTGGCGGGCCTCCCCGCCCTCGTCGTC	480
87	F R P G S R R L L G L G G P P R P F V V	106
481	GTCCTCTCCCCCTGCCAGCCGGCGCCCTCCGGCCGCCAACCGCGCCTCCCCG	540
107	V L L P L A S P G A P P A A P T R A S P	126
541	CTCGGGGCCGTGCGTCCCCGCCGCGTCTCCCTGGCGGCCGGCTCCCGC	600
127	L G A R A S P P R S G V S L A R P A P G	146
<u>SCA2 - A</u>		
601	TGTCCCCGCCGGCGTGCAGGCCGGTATGGCCCTCACATGTCGCTGAAGCCCCAG	660
147	C P R P A C E P V Y G P L T M S L K P Q	166
661	CAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAACAGCAGCAGCAGCAGCAG	720
167	Q Q	186
<u>SCA2 - B</u>		
721	CAGCCGCCGCCGCCGGCTGCCAATGTCGCAAGCCCCGGCGAGCGGCCCTCTAGCGTCG	780
187	Q P P P A A A N V R K P G G S G L L A S	206
781	CCCGCCGCCGCCCTCGCCGTCTCGTCTCGGTCTCTCGTCTCGGCCACGGCTCCC	840
207	P A A A P S P S S S V S S S S A T A P	226
841	TCCTCGGTGGTCCGGCGACCTCCGGCGGGAGGCCGGCTGGCAGAGTCGAAAC	900
227	S S V V A A T S G G G R P G L G R G R N	246
901	AGTAACAAAGGACTGCCTCAGTCTACGATTCTTTGATGGAATCTATGCAAATATGAGG	960
247	S N K G L P Q S T I S F D G I Y A N M R	266
961	ATGGTTCATATACTTACATCAGTTGGCTCAAATGTGAAGTACAAGTGAAGGAA	1020
267	M V H I L T S V V G S K C E V Q V K N G	286
<u>SCA2 - 14B</u>		
1021	GGTATATATGAAGGAGTTTTAAAACCTACAGTCGAAGTGTGATTGGTACTTGATGCC	1080
287	G I Y E G V F K T Y S P K C D L V L D A	306
1081	GCACATGAGAAAAGTACAGAAATCCAGTTGGGGCCGAAACGTGAAGAAATAATGGAGAGT	1140
307	A H E K S T E S S S G P K R E E I M E S	326
1141	ATTTGTTCAAATGTTCAGACTTGGTGTGGTACAGTTAAAGATATGGACTCCAGTTAT	1200
327	I L F K C S D F V V V Q F K D M D S S Y	346
1201	GCAAAAAGAGATGCTTTACTGACTCTGCTATCAGTCTAAAGTGAATGGCAACACAAA	1260
347	A K R D A F T D S A I S A K V N G E H K	366
1261	GAGAAGGACCTGGAGCCCTGGGATGCAGGTGAACTCACAGCCAATGAGGAACCTGAGGCT	1320
367	E K D L E P W D A G E L T A N E E L E A	386
1321	TTGGAAAATGACGTATCTAATGGATGGGATCCCAATGATATGTTCGATATAATGAAGAA	1380
387	L E N D V S N G W D P N D M F R Y N E E	406
1381	AATTATGGTGTAGTGTCTACGTATGATAGCAGTTATCTCGTATACAGTGCCTTAGAA	1440
407	N Y G V V S T Y D S S L S S Y T V P L E	426
1441	AGAGATAACTCAGAAGAATTAAACGGGAAGCAAGGGCAAACCCAGTTAGCAGAAGAA	1500
427	R D N S E E F L K R E A R A N Q L A E E	446

FIGURE 6A

1501	ATTGAGTCAGTGCCCAGTACAAGCTCGAGTGGCCCTGGAAAATGATGATAGGAGTGAG	1560
447	I E S S A Q Y K A R V A L E N D D R S E	466
1561	GAAGAAAAATACACAGCAGTTCAGAGAAATTCCAGTGAACGTGAGGGGCACAGCATAAAC	1620
467	E E K Y T A V Q R N S S E R E G H S I N	486
1621	ACTAGGGAAAATAATATATTCCCTCTGGACAAAGAAATAGAGAAGTCATATCCTGGGA	1680
487	T R E N K Y I P P G Q R N R E V I S W G	506
1681	AGTGGGAGACAGAATTACCCCGTATGGCCAGCCTGGATCGGGCTCCATGCCATCAAGA	1710
507	S G R Q N S P R M G Q P G S G S M P S R	526
1741	TCCACTTCTCACACTTCAGATTCAACCCGAATTCTGGTTAGACCAAAGAGTAGTTAAT	1800
527	S T S H T S D F N P N S G S D Q R V V N	546
1801	GGAGGTGTTCCCTGGCCATCGCCTGGCCATCTCCTCTCGCCCACCTCTCGCTAC	1860
547	G G V P W P S P C P S P S S R P P S R Y	566
1861	CAGTCAGGTCCAACCTCTTCCACCTCGGGCAGCCACCCCTACACGGCCGCCCTCAGG	1920
567	Q S G P N S L P P R A A T P T R P P S R	586
1921	CCCCCCTCGCGGCCATCCAGACCCCCGTCTCACCCCTCTGCTCATGGTTCTCAGCTCC	1980
587	P P S R P S R P P S H P S A H G S P A P	606
1981	GTCTCTACTATGCCTAAACGCATGTCTCAGAAGGGCTCAAGGATGTCCCCAAAGGCC	2040
607	V S T M P K R M S S E G P P R M S P K A	626
2041	CAGCGACATCCTCGAAATCACAGAGTTCTGCTGGAGGGGTTCCATATCCAGTGGCCTA	2100
627	Q R H P R N H R V S A G R G S I S S G L	646
2101	GAATTGTATCCCACAACCCACCCAGTGAAGCAGCTACTCCTCCAGTAGCAAGGACAGT	2160
647	E F V S H N P P S E A A T P P V A R T S	666
2161	CCCTGGGGGGAACGTGGTCATCAGTGGTCAGTGGGTTCCAAGATTATCCCCTAAAAC	2220
667	P S G G T W S S V V S G V P R L S P K T	686
2221	CATAGACCCAGGTCTCCAGACAGAACAGTATTGAAATACCCCCAGTGGCCAGTTCTT	2280
687	H R P R S P R Q N S I G N T P S G P V L	706
2281	GCTTCTCCCCAAGCTGGTATTATTCCAACCTGAAGCTGTTGCCATGCCATTCCAGCTGCA	2340
707	A S P Q A G I I P T E A V A M P I P A A	726
2341	TCTCCTACGCCCTGCTAGTCTGCATCGAACAGAGCTGTTACCCCTCTAGTGAGGCTAA	2400
727	S P T P A S P A S N R A V T P S S E A K	746
2401	GATTCCAGGCTCAAGATCAGAGGGCAGAACTCTCCTGCAGGGATAAAAGAAAATTAAA	2460
747	D S R L Q D Q R Q N S P A G N K E N I K	766
2461	CCCAATGAAACATCACCTAGCTCTCAAAGCTGAAAACAAAGGTATATCACCAGTTGT	2520
767	P N E T S P S F S K A E N K G I S P V V	786
2521	TCTGAACATAGAAAACAGATTGATGATTAAAGAAATTAAAGAATGATTTAGGTTACAG	2580
787	S E H R K Q I D D L K K F K N D F R L Q	806
2581	CCAAGTTCTACTTCTGAATCTATGGATCAACTACTAAACAAAAATAGAGAGGGAGAAAA	2640
807	P S S T S E S M D Q L L N K N R E G E K	826
2641	TCAAGAGATTGATCAAAGACAAAATTGAACCAAGTGTCAAGGATTCTTCATTGAAAAT	2700
827	S R D L I K D K I E P S A K D S F I E N	846
2701	AGCAGCAGCAACTGTACCATGGCAGCAGCAAGCGAATAGCCCCAGCATTTCCCCTCA	2760
847	S S S N C T S G S S K P N S P S I S P S	866
2761	ATACTTAGTAACACGGAGCACAGAGGGGACCTGAGGTCACTTCCCAAGGGGTTAGACT	2820
867	I L S N T E H K R G P E V T S Q G V Q T	886
2821	TCCAGCCCAGCATGTAACAGAGAAAGACGATAAGGAAGAGAAGAAAGACCGAGCTGAG	2880
887	S S P A C K Q E K D D K E E K K D A A E	906
2881	CAAGTTAGGAAATCAACATTGAATCCCAATGCAAAGGAGTTCAACCCACGTTCTCT	2940
907	Q V R K S T L N P N A K E F N P R S F S	926
2941	CAGCCAAAGCCTCTACTACCCCAACTTCACCTCGGCCTCAAGCACAACCTAGCCCAC	3000
927	Q P K P S T T P T S P R P Q A Q P S P S	946
3001	ATGGTGGGTCAACAGCCAACCTCCAGTTATACTCAGCCTGTTGTTGCACCAAT	3060
947	M V G H Q Q P T P V Y T Q P V C F A P N	966
3061	ATGATGTATCCAGTCCAGTGAGCCAGGCAGTCACCCAT	3120
967	M M Y P V P V S P G V Q P L Y P I P M T	986

3121	CCCATGCCAGTGAATCAAGCCAAGACATATAGAGCAGTACCAAATATGCCCAACAGCGG	3180
987	P M P V N Q A K T Y R A V P N M P Q Q R	1006
3181	CAAGACCAGCATCATCAGAGTGCCATGATGCACCCAGCGTCAGCAGGGGCCACCGATT	3240
1007	Q D Q H H Q S A M M H P A S A A G P P I	1026
3241	GCAGCCACCCCCACCAGCTTACTCCACGCAATATGTTGCCTACAGTCCTCAGCAGTTCCA	3300
1027	A A T P P A Y S T Q Y V A Y S P Q Q F P	1046
3301	AATCAGCCCCCTGTTCAGCATGTGCCACATTATCAGTCTCAGCATCCTCATGTCATAGT	3360
1047	N Q P L V Q H V P H Y Q S Q H P H V Y S	1066
3361	CCTGTAATAACAGGGTAATGCTAGAATGATGGCACCAACACAGCCCAGCCTGGTTA	3420
1067	P V I Q G N A R M M A P P T H A Q P G L	1086
3421	GTATCTTCTTCAGCAACTCAGTACGGGCTCATGAGCAGACGCATGCGATGTATGCATGT	3480
1087	V S S S A T Q Y G A H E Q T H A M Y A C	1106
3481	CCCAAATTACCATACAACAAGGAGACAAGCCCTTCTTCTACTTGCCTTTACACGGGC	3540
1107	P K L P Y N K E T S P S F Y F A I S T G	1126
3541	TCCCTTGCTCAGCAGTATGGCACCCCTAACGCTACCCCTGCACCCACATACTCCACACCC	3600
1127	S L A Q Q Y A H P N A T L H P H T P H P	1146
3601	CAGCCTTCAGCTACCCCCACTGGACAGCAGCAAAGCCAACATGGTGGAAAGTCATCCTGCA	3660
1147	Q P S A T P T G Q Q Q S Q H G G S H P A	1166
3661	CCCAGTCCTGTTAGCACCACATCAGCACCCAGGCCAGGCTCTCCATCTGGCAGTCCA	3720
1167	P S P V Q H H Q H Q A A Q A L H L A S P	1186
3721	CAGCAGCAGTCAGCCATTACCGCGGGCTTGCGCCACTCCACCCCTCATGACACCT	3780
1187	Q Q Q S A I Y H A G L A P T P P S M T P	1206
3781	GCCTCCAACACGCAGTCGCCACAGAAATAGTTCCAGCAGCACAAACAGACTGTTACG	3840
1207	A S N T Q S P Q N S F P A A Q Q T V F T	1226
3841	ATCCATCCTTCTACGTTAGCCGGGTATACCAACCCACCCACATGGCCCACGTACCT	3900
1227	I H P S H V Q P A Y T N P P H M A H V P	1246
3901	CAGGCTCATGTACAGTCAGGAATGGTTCTCTCATCCAACTGCCCATGCGCAATGATG	3960
1247	Q A H V Q S G M V P S H P T A H A P M M	1266
3961	CTAATGACGACACAGCCACCCGGCGGTCCCCAGGCCCTCGCTCAAAGTGCACACTACAG	4020
1267	L M T T Q P P G G P Q A A L A Q S A L Q	1286
4021	CCCATTCCAGTCTCGACAAACAGCGCATTCCCTATATGACGCACCCCTCAGTACAAGCC	4080
1287	P I P V S T T A H F P Y M T H P S V Q A	1306
4081	CACCAACAGCAGTTGTAAGGCTGCCCTGGAGGAACCGAAAGGCCAATTCCCTCCTC	4140
1307	H H Q Q L *	1326
4141	CCTTCTACTGCTTCTACCAACTGGAAGCACAGAAAATAGAATTCTATTATTTGTTT	4200
4201	TAAAATATATATGTTGATTCTTGTAACATCCAATAGGAATGCTAACAGTTCACTGCAG	4260
4261	TGGAAGATACTTGGACCGAGTAGAGGCATTAGGAACCTGGGGCTATTCCATAATTCCA	4320
4321	TATGCTGTTCAAGTCCCGCAGGTACCCCAGCTCTGCTTGCGAAACTGGAAGTTATTT	4380
4381	ATTTTTAATAACCCCTGAAAGTCATGAACACATCAGCTAGCAAAGAAGTAACAAGAGT	4440
4441	GATTCTGCTGCTATTACTGCTAAAAAAAAAAAAAAA 4481	

FIGURE 6C

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Ataxin-2	1	50			
Mouse Ataxin-2	VYGPLTMSLK	PQQQQQQQQQQ	QQQQQQQQQQ	QQQPPPPAAAN	VRKPGGSGLL
A2RP	HEGPLTMSLK	PQPQ.....	PPAPAT GRKPGG.GLL
ConsensusLA	PQPPPPQQHQ	ER.....
Ataxin-2	51	100			
Mouse Ataxin-2	ASPAAPSPS	SSSVSSSAT	APSSVVA...	ATSGGGRPGL	GRGRNSNKGL
A2RP	SSPGAAP.AS	AAVTSASVVP	APAAPVASSS	AAAGGGRPGL	GRGRNSSKGL
Consensus	..PGAAAIGS	A.....	RGQSTGKGP
Ataxin-2	101	150			
Mouse Ataxin-2	PQSTISFDGI	YANMRMVHIL	TSVVGSKCEV	QVKNGGIYEG	VFKTYSPKCD
A2RP	PQPTISFDGI	YANVRMVHIL	TSVVGSKCEV	QVKNGGIYEG	VFKTYSPKCD
Consensus	PQSPV.FEGV	YNNNSRMLHFL	TAVVGSTCDV	KVKNGTTYEG	IFKTLSSKFE
Ataxin-2	151	200			
Mouse Ataxin-2	LVLDAAHEKS	TESSSGPKRE	EIMESILFKC	SDFVVVQFKD	MDSSYAKRDA
A2RP	LVLDAAHEKS	TESSSGPKRE	EIMESVLFKC	SDFVVVQFKD	TDSSYARRDA
Consensus	LAVDAVHRKA	SEPAGGPREE	DIVDTMVFKP	SDVMLVHFRN	VDFNYATKDK
Ataxin-2	201	250			
Mouse Ataxin-2	FTDSAIS..A	KVNGEHKEKD	LEPWDAGELT	ANEELEALEN	DVSNGWDPND
A2RP	FTDSALS..A	KVNGEHKEKD	LEPWDAGELT	ASEELE.LEN	DVSNGWDPND
Consensus	FTDSAIAMNS	KVNGEHKEKV	LQRWEGGD.S	NSDDYD.LES	DMSNGWDPNE
Ataxin-2	251	300			
Mouse Ataxin-2	MFRYNEENYG	VVSTYDSSL	SYTVPLERDN	SEEFLKREAR	ANQLAEEIES
A2RP	MFRYNEENYG	VVSTYDSSL	SYTVPLERDN	SEEFLKREAR	ANQLAEEIES
Consensus	MFKFNEENYG	VKTTYDSSL	SYTVPLEKD	SEEFRQRELR	AAQLAREIES
Ataxin-2	301	350			
Mouse Ataxin-2	MF--NEENYG	V--TYDSSL	SYTVPLE-DN	SEEF--RE-R	A-QLA-EIES
A2RP	SAQYKARVAL	ENDD.RSEEE	KYTAVQRNSS	EREGHSINTR	ENKYIPPGQR
Consensus	SAQYKARVAL	ENDD.RSEEE	KYTAVQRNCS	DREGHGPNT	DNKYIPPGQR
Ataxin-2	351				
Mouse Ataxin-2	NR				
A2RP	NR				
Consensus	..				

FIGURE 7